OIPE 3502 06/19

RAW SEQUENCE LISTING DATE: 06/29/2001
PATENT APPLICATION: **US/09/811,045A** TIME: 12:17:00

Input Set : **A:\D6386D_SEQ.txt**
Output Set: **N:\CRF3\06292001\I811045A.raw**

ENTERED

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 2 <110> APPLICANT: Scott, Robert E.
 4 <120> TITLE OF INVENTION: cDNA encoding P2P proteins and use of P2P cDNA-
 5       derived antibodies and antisense reagents
 6       in determining the proliferative potential of
 7       normal, abnormal and cancer cells in animals
 8       and humans
10 <130> FILE REFERENCE: D6386D
12 <140> CURRENT APPLICATION NUMBER: US 09/811,045A
13 <141> CURRENT FILING DATE: 2001-03-16
14 <150> PRIOR APPLICATION NUMBER: US 08/801,308
15 <151> PRIOR FILING DATE: 1997-02-18
17 <160> NUMBER OF SEQ ID NOS: 4
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1404
21 <212> TYPE: PRT
22 <213> ORGANISM: Unknown
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26 <221> NAME/KEY: PEPTIDE
27 <223> OTHER INFORMATION: P2P polypeptide
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32 Asn Thr Gly Lys Tyr Ala Ile Pro Thr Ile Asp Ala Glu Ala Tyr
33                 20                  25                  30
34 Ala Ile Gly Lys Lys Glu Lys Pro Pro Phe Leu Pro Glu Glu Pro
35                 35                  40                  45
36 Ser Ser Ser Ser Glu Glu Asp Asp Pro Ile Pro Ala Glu Leu Leu
37                 50                  55                  60
38 Cys Leu Ile Cys Lys Asp Ile Met Thr Asp Ala Val Val Ile Pro
39                 65                  70                  75
40 Cys Cys Gly Asn Ser Ser Cys Asp Glu Cys Ile Arg Thr Thr Leu
41                 80                  85                  90
42 Leu Glu Ser Asp Lys His Thr Cys Pro Thr Cys His Gln Asn Asp
43                 95                 100                 105
44 Val Ser Pro Asp Ala Leu Ile Ala Asn Lys Phe Leu Arg Gln Ala
45                110                 115                 120
46 Val Asn Asn Phe Lys Asn Glu Thr Gly Tyr Thr Lys Arg Leu Arg
47                125                 130                 135
48 Lys Gln Leu Pro Pro Phe Leu Phe Leu Val Pro Pro Pro Arg Pro
49                140                 145                 150
50 Leu Ser Gln Arg Asn Leu Gln Pro Arg Ser Arg Ser Pro Ile Leu
51                155                 160                 165
52 Arg Gln Gln Asp Pro Val Val Phe Arg Tyr Thr Val Ser Pro Thr
53                170                 175                 180
54 Cys Ser Asp Thr Lys Thr Ala Gly Ser Cys Ser Asp Ser Gly Thr
55                185                 190                 195
56 Leu Ser Arg Leu Pro Ala Pro Ser Ile Ser Ser Leu Thr Ser Asn
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                200                 205                 210
Gln Ser Ser Leu Ala Pro Pro Val Ser Gly Asn Pro Ser Ser Ala
                215                 220                 225
Pro Ala Pro Val Pro Asp Ile Thr Ala Thr Val Ser Ile Ser Val
                230                 235                 240
His Ser Glu Lys Ser Asp Gly Pro Phe Arg Asp Ser Asp Asn Lys
                245                 250                 255
Leu Leu Pro Ala Ala Ala Leu Thr Ser Glu His Ser Lys Gly Ala
                260                 265                 270
Ser Ser Ile Ala Ile Thr Ala Leu Met Glu Glu Lys Gly Val Pro
                275                 280                 285
Gly Thr Ser Pro Trp Asn Ser Ile Phe Val Gly Gln Ser Leu Leu
                290                 295                 300
His Gly Gln Leu Ile Pro Thr Thr Gly Pro Val Arg Ile Asn Ala
                305                 310                 315
Ala Arg Pro Gly Gly Gly Arg Pro Gly Trp Glu His Ser Asn Lys
                320                 325                 330
Leu Gly Tyr Leu Val Ser Pro Pro Gln Gln Ile Arg Arg Gly Glu
                335                 340                 345
Arg Ser Cys Tyr Arg Ser Ile Asn Arg Gly Arg His His Ser Glu
                350                 355                 360
Arg Ser Gln Arg Thr Gln Ser Pro Ser Leu Pro Ala Thr Pro Cys
                365                 370                 375
Phe Val Pro Val Pro Pro Pro Pro Leu Tyr Pro Pro Pro Pro His
                380                 385                 390
Thr Leu Pro Leu Pro Pro Gly Val Pro Pro Pro Gln Phe Ser Pro
                395                 400                 405
Gln Phe Pro Ser Ser Gln Pro Pro Thr Ala Gly Tyr Ser Val Pro
                410                 415                 420
Pro Pro Gly Phe Pro Pro Ala Pro Ala Asn Ile Ser Thr Ala Cys
                425                 430                 435
Phe Ser Pro Gly Val Pro Thr Ala His Ser Asn Thr Met Pro Thr
                440                 445                 450
Thr Gln Ala Pro Leu Leu Ser Arg Glu Glu Phe Tyr Arg Glu Gln
                455                 460                 465
Asn Asp Lys Gly Arg Glu Ser Lys Phe Pro Tyr Ser Gly Ser Ser
                470                 475                 480
Tyr Ser Arg Ser Ser Tyr Thr Asp Ser Ser Gln Gly Leu Ala Gln
                485                 490                 495
His Ile His Ala Leu Thr Leu Ser Pro Ser Ala Ala His Thr Leu
                500                 505                 510
Asp Leu Leu His Asp His Pro His Pro Pro Glu Glu Ala Glu Ala
                515                 520                 525
Arg Ser Ala Met Ile Val His Met Pro Asp Leu Met Asp Ile Ala
                530                 535                 540
His Ala Arg Ser Arg Ser Pro Pro Tyr Arg Arg Tyr Arg Ser Arg
                545                 550                 555
Ser Arg Ser Pro Pro Glu Phe Arg Gly Gln Ser Pro Thr Lys Arg
                560                 565                 570
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106 Asn Val Pro Arg Glu Glu Lys Glu Arg Glu Tyr Phe Asn Arg Tyr
107 575 580 585
108 Arg Glu Val Pro Pro Pro Tyr Asp Ile Lys Ala Tyr Tyr Gly Arg
109 590 595 600
110 Ser Val Asp Phe Arg Asp Pro Phe Glu Lys Glu Arg Tyr Arg Glu
111 605 610 615
112 Trp Glu Arg Lys Tyr Arg Glu Trp Tyr Glu Lys Tyr Tyr Lys Gly
113 620 625 630
114 Tyr Ala Val Gly Ala Gln Pro Arg Pro Ser Ala Asn Arg Glu Asp
115 635 640 645
116 Phe Ser Pro Glu Arg Leu Leu Pro Leu Asn Ile Arg Asn Ser Pro
117 650 655 660
118 Phe Thr Arg Gly Arg Arg Glu Asp Tyr Ala Ala Gly Gln Ser His
119 665 670 675
120 Arg Asn Arg Asn Leu Gly Gly Asn Tyr Pro Glu Lys Leu Ser Thr
121 680 685 690
122 Arg Asp Ser His Asn Ala Lys Asp Asn Pro Lys Ser Lys Glu Lys
123 695 700 705
124 Glu Ser Glu Asn Val Pro Gly Asp Gly Lys Gly Asn Lys His Lys
125 710 715 720
126 Lys His Arg Lys Arg Arg Asn Glu Glu Lys Gly Glu Glu Ser Glu
127 725 730 735
128 Ser Phe Leu Asn Pro Glu Leu Leu Glu Thr Ser Arg Lys Cys Arg
129 740 745 750
130 Gly Ser Ser Gly Ile Asp Glu Thr Lys Thr Asp Thr Leu Phe Val
131 755 760 765
132 Leu Pro Ser Arg Asp Asp Ala Thr Pro Val Arg Asp Glu Pro Met
133 770 775 780
134 Asp Ala Glu Ser Ile Thr Phe Lys Ser Val Ser Asp Lys Asp Lys
135 785 790 795
136 Arg Glu Lys Asp Lys Pro Lys Val Lys Ser Asp Lys Thr Lys Arg
137 800 805 810
138 Lys Ser Asp Gly Ser Ala Thr Ala Lys Lys Asp Asn Val Leu Lys
139 815 820 825
140 Pro Ser Lys Gly Pro Gln Glu Lys Val Asp Gly Asp Arg Glu Lys
141 830 835 840
142 Ser Pro Arg Ser Glu Pro Pro Leu Lys Lys Ala Lys Glu Glu Ala
143 845 850 855
144 Thr Lys Ile Asp Ser Val Lys Pro Ser Ser Ser Ser Gln Lys Asp
145 860 865 870
146 Glu Lys Val Thr Gly Thr Pro Arg Lys Ala His Ser Lys Ser Ala
147 875 880 885
148 Lys Asp Thr Arg Arg Gln Ser Gln Pro Arg Thr Arg Arg Ser Lys
149 890 895 900
150 Arg Thr Val Pro Lys Thr Ser Ser Gln Lys Ser Gln Pro Val Arg
151 905 910 915
152 Thr Arg Arg Pro Arg Ser Leu Arg Lys Ile Asn Tyr Leu Ile Ala
153 920 925 930
154 Arg Glu Lys Asn Glu Arg Glu Lys Arg Lys Lys Ser Val Asp Lys

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156 Asp Phe Glu Ser Ser Ser Met Lys Ile Ser Lys Val Glu Gly Thr
157                 950                 955                 960
158 Glu Ile Val Lys Pro Ser Pro Lys Arg Lys Met Glu Gly Asp Val
159                 965                 970                 975
160 Glu Lys Leu Glu Arg Thr Pro Glu Lys Asp Lys Ile Ala Ser Ser
161                 980                 985                 990
162 Thr Thr Pro Ala Lys Lys Ile Lys Leu Asn Arg Glu Thr Gly Lys
163                 995                1000                1005
164 Lys Ile Gly Asn Ala Glu Asn Ala Ser Thr Thr Lys Glu Pro Ser
165                1010                1015                1020
166 Glu Lys Leu Glu Ser Thr Ser Ser Lys Ile Lys Gln Glu Lys Val
167                1025                1030                1035
168 Lys Gly Lys Ala Lys Arg Lys Val Ala Gly Ser Glu Gly Ser Ser
169                1040                1045                1050
170 Ser Thr Leu Val Asp Tyr Thr Ser Thr Ser Ser Thr Gly Gly Ser
171                1055                1060                1065
172 Pro Val Arg Lys Ser Glu Glu Lys Thr Asp Thr Lys Arg Thr Val
173                1070                1075                1080
174 Ile Lys Thr Met Glu Glu Tyr Asn Asn Asp Asn Thr Ala Pro Ala
175                1085                1090                1095
176 Glu Asp Val Ile Ile Met Ile Gln Val Pro Gln Ser Lys Trp Asp
177                1100                1105                1110
178 Lys Asp Asp Phe Glu Ser Glu Glu Glu Asp Val Lys Thr Thr Gln
179                1115                1120                1125
180 Pro Ile Gln Ser Val Gly Lys Pro Ser Ser Ile Ile Lys Asn Val
181                1130                1135                1140
182 Thr Thr Lys Pro Ser Ala Thr Ala Lys Tyr Thr Glu Lys Glu Ser
183                1145                1150                1155
184 Glu Gln Pro Glu Lys Leu Gln Lys Leu Pro Lys Glu Ala Ser His
185                1160                1165                1170
186 Glu Leu Met Gln His Glu Leu Arg Ser Ser Lys Gly Ser Ala Ser
187                1175                1180                1185
188 Ser Glu Lys Gly Arg Ala Lys Asp Arg Glu His Ser Gly Ser Glu
189                1190                1195                1200
190 Lys Asp Asn Pro Asp Lys Arg Lys Ser Gly Ala Gln Pro Asp Lys
191                1205                1210                1215
192 Glu Ser Thr Val Asp Arg Leu Ser Glu Gln Gly His Phe Lys Thr
193                1220                1225                1230
194 Leu Ser Gln Ser Ser Lys Glu Thr Arg Thr Ser Glu Lys His Glu
195                1235                1240                1245
196 Ser Val Arg Gly Ser Ser Asn Lys Asp Phe Thr Pro Gly Arg Asp
197                1250                1255                1260
198 Lys Lys Val Asp Tyr Asp Ser Arg Asp Tyr Ser Ser Ser Lys Arg
199                1265                1270                1275
200 Arg Asp Glu Arg Gly Glu Leu Ala Arg Arg Lys Asp Ser Pro Pro
201                1280                1285                1290
202 Arg Gly Lys Glu Ser Leu Ser Gly Gln Lys Ser Lys Leu Arg Glu
203                1295                1300                1305
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204 Glu Arg Asp Leu Pro Lys Lys Gly Ala Glu Ser Lys Lys Ser Asn
205                 1310                1315                1320
206 Ser Ser Pro Pro Arg Asp Lys Lys Pro His Asp His Lys Ala Pro
207                 1325                1330                1335
208 Tyr Glu Thr Lys Arg Pro Cys Glu Glu Thr Lys Pro Val Asp Lys
209                 1340                1345                1350
210 Asn Ser Gly Lys Glu Arg Glu Lys His Ala Ala Glu Ala Arg Asn
211                 1355                1360                1365
212 Gly Lys Glu Ser Ser Gly Ala Asn Cys His Val Tyr Leu Thr Arg
213                 1370                1375                1380
214 Gln Thr Leu Pro Trp Arg Arg Ser Trp Leu Leu Gly Arg Trp Arg
215                 1385                1390                1395
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217                 1400
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227 <223> OTHER INFORMATION: P2P cDNA
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232 ggaattccta gaagttttat gatggaagtg aaagatccta acatgaaagg tgcaatgctt 180
233 accaacactg gaaaatatgc aataccaact atagatgcag aggcctatgc aatcgggaag 240
234 aaagagaaac cacccttctt accagaggag ccatcatcat cttcagaaga agatgatcct 300
235 atcccagcag agctcttgtg cctcatctgc aaagacatca tgactgatgc tgtggtcatt 360
236 ccctgctgtg gaaacagttc atgtgatgaa tgtataagaa cgacactctt ggagtcagat 420
237 aaacatacat gtccaacatg tcaccaaaat gatgtttctc ctgatgcttt aattgccaac 480
238 aagtttttac gacaggctgt taataacttt aaaaatgaaa ctggctatac aaaacgacta 540
239 cgaaaacagt tacctccatt tttatttttа gtaccaccac caagaccact cagtcagcgg 600
240 aacctacagc ctcgtagtag atctccaata ctaagacagc aggatcctgt agtattcagg 660
241 tacactgtct cgcctacctg ctccgatact aagacagcag gatcctgtag tgattcaggt 720
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244 accgtgtcta tatcagtcca ctcagaaaaa tcggatggac cttttcggga ttctgataat 900
245 aaattattgc cagctgccgc ccttacatca gaacattcaa agggagcctc ttcaattgct 960
246 attactgctc ttatggaaga aaaaggggta ccaggtacca gtccttggaa ctccatcttt 1020
247 gttggacagt cattattaca tggacagttg attcccacaa ctggcccagt aagaatcaat 1080
248 gctgctcgtc caggtggtgg ccggccaggc tgggagcatt ccaacaagct tgggtaccta 1140
249 gtttctccac cacagcaaat tagaagagga gaaagaagct gttacagaag tataaaccgc 1200
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253 gcaggatata gtgtccctcc tccaggattt ccaccagctc ctgccaatat atcaacagct 1440
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255 cttttgtcca gggaagaatt ctatagagag caaaacgaca aaggaagaga gtctaaattt 1560
256 ccctatagtg ggtcatcgta ttcaagaagt tcatacactg actcaagtca aggtctggct 1620
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VERIFICATION SUMMARY DATE: 06/29/2001
PATENT APPLICATION: **US/09/811,045A** TIME: 12:17:01

Input Set : **A:\D6386D_SEQ.txt**
Output Set: **N:\CRF3\06292001\I811045A.raw**

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